Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	9	(Goldberg NEAR Edward) AND (phage OR bacteriophage)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/03 13:51
L4	14	NANOFRAMES	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/03 13:58
L5	11	(bacteriophage WITH tail) and (p35 OR gp35)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/03 14:00
L6	20	bacteriophage (p35 OR gp35)	US-PGPUB; USPAT; EPO; JPO; DERWENT	SAME	ON	2005/05/03 14:02
L7	9	bacteriophage (p35 OR gp35)	US-PGPUB; USPAT; EPO; JPO; DERWENT	WITH	ON	2005/05/03 14:02
S1	685	Goldberg NEAR Edward	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2003/12/09 14:01
S2	23544	bacteriophage	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2003/12/09 14:04
S3	7223	bacteriophage and tail	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2003/12/09 14:04
S4	5	(US-5877279-$ or US-6437112-$ or US-5864013-$).did. or (WO-9611947-$).did. or (WO-200077196-$).did.	USPAT; EPO; DERWENT	OR	OFF	2003/12/09 19:41
S5	8	(Goldberg NEAR Edward) and phage	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/03 13:51
S6	8	(Goldberg NEAR Edward) and bacteriophage	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/10/12 17:33
S7	10	(bacteriophage and tail) and gp35	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/03 13:56
S8	7	gp35 WITH isolated	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/10/12 17:34

S9	9	gp35 WITH purified	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/10/12 17:35
S10	19	gp35 WITH protein	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/10/12 17:36

(FILE 'HOME' ENTERED AT 12:38:48 ON 03 MAY 2005)

FILE 'MEDLINE, CANCERLIT, AGRICOLA, CAPLUS, SCISEARCH' ENTERED AT 12:39:20 ON 03 MAY 2005

L1 95095 S BACTERIOPHAGE
L2 13 S L1 AND (T4 (L) GP35)
L3 8 DUP REM L2 (5 DUPLICATES REMOVED)
L4 8 SORT L3 PY

=> d an ti so au ab pi l4 1-8

L4 ANSWER 1 OF 8 MEDLINE on STN
AN 82127583 MEDLINE
TI Organization of the **bacteriophage** T4 tail fiber gene cluster 34-38.
SO Progress in clinical and biological research, (1981) 64 353-64. Journal code: 7605701. ISSN: 0361-7742.
AU Revel H R
AB A correlation of the genetic, functional, and structural maps of the **T4** tail fiber gene cluster has been achieved by analysis of lambda derivatives carrying genes 34-38. 31 recombinants carrying different parts of the **T4** tail fiber gene cluster were identified by a marker rescue screen of 300 lambda **T4** recombinant clones, generated by restriction of partial cytosine-containing **T4** DNA with E coRI or with HindIII and ligation into appropriately cleaved lambda replacement vectors. Extensive genetic characterization revealed 15 recombinant classes with respect to the contiguous stretches of genome recovered and suggested the presence of 7 HindIII sites and 8 EcoRI sites in the 10 kb region. Functional analysis showed tht genes 34-38 were recovered intact. The tail fiber genes are efficiently expressed from lambda promoters and complement **T4** amber mutants in a modified in vivo complementation test. Polypeptides, Mr = 145,000, 105,000, 39,000, 27,000 and 24,000 corresponding to gp34, gp37, **gp35**, gp38 and gp36 respectively, were detected by SDS polyacrylamide gel electrophoresis of 35S- labeled extracts of lambda **T4** recombinant infected UV-treated host cells. Restriction enzyme structural analysis of the lambda **T4** DNAs identified 7 HindIII and 7 EcoRI fragments and established a restriction map covering about 11 kb. The correlation of the genetic, functional and restriction maps provides a rational approach to a genetically directed DNA sequence analysis of the **T4** tail fiber genes and of their mutant variants which affect particular aspects of tail fiber assembly, structure and function.

L4 ANSWER 2 OF 8 MEDLINE on STN
AN 96326707 MEDLINE
TI Stoichiometry and domainal organization of the long tail-fiber of **bacteriophage** T4: a hinged viral adhesin.
SO Journal of molecular biology, (1996 Aug 2) 260 (5) 767-80. Journal code: 2985088R. ISSN: 0022-2836.
AU Cerritelli M E; Wall J S; Simon M N; Conway J F; Steven A C
AB The long-tail fibers (LTFs) form part of **bacteriophage T4**'s apparatus for host cell recognition and infection, being responsible for its initial attachment to susceptible bacteria. The LTF has two parts, each approximately 70 to 75 nm long; gp34 (140 kDa) forms the proximal half-fiber, while the distal half-fiber is composed of gp37 (109 kDa), gp36(23 kDa) and **gp35** (30 kDa). LTFs have long been thought to be dimers of gp34, gp37 and gp36, with one copy of **gp35**. We have used mass mapping by scanning transmission electron microscopy (STEM), quantitative SDS-PAGE, and computational sequence analysis to study the structures of purified LTFs and half-fibers of both kinds. These data establish that the LTF is, in fact, trimeric, with a stoichiometry of gp34: gp37: gp36: **gp35** = 3:3:3:1. Averaged images of stained and unstained molecules resolve the LTF into a linear stack of 17 domains. At the proximal end is a globular domain of approximately 145 kDa that becomes incorporated into the baseplate. It is followed by a rod-like shaft (33 x 4 mm; 151 kDa) which correlates with a cluster of seven quasi repeats, each 34 to 39 residues long. The proximal half-fiber terminates in three globular domains. The distal half-fiber consists of ten globular domains of variable size and spacing, preceding a needle-like end domain (15 x 2.5 nm; 31 kDa). The LTF is rigid apart from

hinges between the two most proximal domains, and between the proximal and distal half-fibers. The latter hinge occurs at a site of local non-equivalence (the "kneecap") at which density, correlated with the presence of **gp35**, bulges asymmetrically out on one side. Several observations indicate that gp34 participates in the sharing of conserved structural modules among coliphage tail-fiber genes to which gp37 was previously noted to subscribe. Two adjacent globular domains in the proximal half-fiber match a pair of domains in the distal half-fiber, and the rod domain in the proximal half-fiber resembles a similar domain in the **T4** short tail-fiber (gp12). Finally, possible structures are considered; combining our data with earlier observations, the most likely conformation for most of the LTF is a three-stranded beta-helix.

L4 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1996:404766 CAPLUS
DN 125:51926
TI Tail fiber proteins of T-even-like **bacteriophage** for the production of nanometer structures and use thereof
SO PCT Int. Appl., 82 pp.
CODEN: PIXXD2
IN Goldberg, Edward B.
AB Described is the preparation of nanostructures, i.e., nanometer sized structures useful in the construction of microscopic and macroscopic structures, based on **bacteriophage T4** tail fiber proteins and variants thereof. Preparation of single or fusion proteins or their variants selected from gp34, **gp35**, gp36, and gp37 of T-4 **bacteriophage** was demonstrated. Also provided are kits for making nanostructures, comprising purified, e.g., **gp35** and gp36-34 chimer, or gp37-36 chimer.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9611947	A1	19960425	WO 1995-US13023	19951013
W: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5877279	A	19990302	US 1994-322760	19941013
CA 2202474	AA	19960425	CA 1995-2202474	19951013
AU 9538296	A1	19960506	AU 1995-38296	19951013
AU 689662	B2	19980402		
EP 785946	A1	19970730	EP 1995-936297	19951013
EP 785946	B1	20041229		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
BR 9509487	A	19970930	BR 1995-9487	19951013
CN 1168676	A	19971224	CN 1995-196597	19951013
CN 1113068	B	20030702		
HU 77683	A2	19980728	HU 1998-746	19951013
JP 10508194	T2	19980818	JP 1996-513358	19951013
RU 2162856	C2	20010210	RU 1997-107477	19951013
AT 286068	E	20050115	AT 1995-936297	19951013

L4 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1999:69916 CAPLUS
DN 130:135644
TI Use of **bacteriophage** T4 tail fiber proteins in the preparation of nanostructures
SO U.S., 51 pp., Cont.-in-part of U.S. Ser. No. 322,760.
CODEN: USXXAM
IN Goldberg, Edward B.
AB Methods of using the gp34, **gp35**, gp36, and gp37 tail fiber proteins of **bacteriophage T4** in the formation of nanostructures that can be used in nanomachines is described. In particular, variants of the proteins that show altered patterns of interaction, thermolability of interaction, or geometry of interaction can be used to create an array of self-assembling structures.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 5864013	A	19990126	US 1995-542003	19951012

US 5877279	A	19990302	US 1994-322760	19941013
CA 2202474	AA	19960425	CA 1995-2202474	19951013
CN 1168676	A	19971224	CN 1995-196597	19951013
CN 1113068	B	20030702		
HU 77683	A2	19980728	HU 1998-746	19951013
US 6437112	B1	20020820	US 1999-236949	19990125
US 2003236390	A1	20031225	US 2002-136225	20020429
US 2004018587	A1	20040129	US 2003-371067	20030221
US 2004039168	A1	20040226	US 2003-371073	20030221

L4 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2000:900798 CAPLUS
DN 134:67178
TI Cloning and characterization of phage **T4** gene **gp35**
SO PCT Int. Appl., 75 pp.
CODEN: PIXXD2
IN Goldberg, Edward B.
AB The invention provides sequences of phage **T4** gene **gp35** and its encoded protein and cDNA sequences of a novel human gene which is located between gene gp34 and gene gp36. Gene **gp35** encodes a tail fiber protein which functions to join the rodlike proximal and distal halves of the **bacteriophage** tail fibers. A thermostable **gp35** mutant protein is also isolated from a ts mutant. The present invention further relates to the use of **bacteriophage** **T4** **gp35** gene and protein products as well as derivs., variants, and analogs thereof in the construction of nanostructures.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000077196	A1	20001221	WO 1999-US13024	19990611
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2375998	AA	20001221	CA 1999-2375998	19990611
AU 9946781	A1	20010102	AU 1999-46781	19990611
EP 1185638	A1	20020313	EP 1999-930192	19990611
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003507007	T2	20030225	JP 2001-503640	19990611

L4 ANSWER 7 OF 8 MEDLINE on STN
AN 2004603885 MEDLINE
TI In vivo bypass of chaperone by extended coiled-coil motif in T4 tail fiber.
SO Journal of bacteriology, (2004 Dec) 186 (24) 8363-9.
Journal code: 2985120R. ISSN: 0021-9193.
AU Qu Yun; Hyman Paul; Harrah Timothy; Goldberg Edward
AB The distal-half tail fiber of **bacteriophage** **T4** is made of three gene products: trimeric gp36 and gp37 and monomeric **gp35** . Chaperone P38 is normally required for folding gp37 peptides into a P37 trimer; however, a temperature-sensitive mutation in **T4** (ts3813) that suppresses this requirement at 30 degrees C but not at 42 degrees C was found in gene 37 (R. J. Bishop and W. B. Wood, Virology 72:244-254, 1976). Sequencing of the temperature-sensitive mutant revealed a 21-bp duplication of wild-type gene 37 inserted into its C-terminal portion (S. Hashemolhosseini et al., J. Mol. Biol. 241:524-533, 1994). We noticed that the 21-amino-acid segment encompassing this duplication in the ts3813 mutant has a sequence typical of a coiled coil and hypothesized that its extension would relieve the temperature sensitivity of the ts3813 mutation. To test our hypothesis, we crossed the **T4** ts3813 mutant with a plasmid encoding an engineered pentaheptad coiled coil. Each of the six mutants that we examined retained two amber mutations in gene 38 and had a different coiled-coil sequence varying from three to five heptads. While the sequences varied, all maintained the heptad-repeating coiled-coil motif and produced plaques at up to 50 degrees C. This finding strongly suggests that the coiled-coil motif is a critical factor in the folding of gp37. The presence of a terminal coiled-coil-like sequence in the tail fiber genes of 17 additional T-even phages implies the conservation of this mechanism. The increased melting temperature should be useful for "clamps" to initiate the folding of trimeric beta-helices in vitro and as an in vivo screen to identify, sequence, and characterize trimeric coiled coils.

L4 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:162508 CAPLUS
DN 140:213583
TI Use of **bacteriophage** T4 tail fiber proteins for manufacture of nanostructures using staged-assembly
SO U.S. Pat. Appl. Publ., 60 pp., Cont.-in-part of U.S. Ser. No. 136,225.
CODEN: USXXCO
IN Goldberg, Edward B.
AB Methods of using the gp34, **gp35**, gp36, and gp37 tail fiber proteins of **bacteriophage T4** or fusion proteins in the formation of nanostructures that can be used in nanostructures is described. In particular, variants of the proteins that show altered patterns of interaction, thermolability of interaction, or geometry of interaction can be used to create an array of self-assembling structures.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2004039168	A1	20040226	US 2003-371073	20030221
US 5877279	A	19990302	US 1994-322760	19941013
US 5864013	A	19990126	US 1995-542003	19951012
US 6197139	B1	20010306	US 1999-226949	19990108
US 2003236390	A1	20031225	US 2002-136225	20020429

L7 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1973:544087 CAPLUS
DN 79:144087
TI Assembly of **Bacteriophage** T4 tail fibers. IV. Subunit composition of tail fibers and fiber precursors
SO Journal of Molecular Biology (1973), 79(4), 633-47
CODEN: JMOBAK; ISSN: 0022-2836
AU Dickson, Robert C.
AB Using a novel purification procedure, the protein composition of the tail fibers of **bacteriophage T4** has been determined Fibers contain 4 proteins whose mol. wts. as estimated by Na dodecyl sulfate-acrylamide gel electrophoresis, are 150,000; 125,000; 40,000; and 24,000. The 2 largest proteins have been previously identified as the products of genes 34 (P34) and 37(P37), resp. The 2 smaller proteins have now been identified as the products of genes 35 (P35) and 36 (P36), resp. The products of the 2 other known phage genes required for fiber assembly, 38 and 57, have been identified as nonstructural phage proteins with mol. wts. of 26,000 and 10,000 resp.

=> d his

(FILE 'HOME' ENTERED AT 12:38:48 ON 03 MAY 2005)

FILE 'MEDLINE, CANCERLIT, AGRICOLA, CAPLUS, SCISEARCH' ENTERED AT 12:39:20 ON 03 MAY 2005

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L1         95095 S BACTERIOPHAGE
L2            13 S L1 AND (T4 (L) GP35)
L3             8 DUP REM L2 (5 DUPLICATES REMOVED)
L4             8 SORT L3 PY
L5            14 S L1 AND (T4 (L) (P35 OR GP35))
L6             9 DUP REM L5 (5 DUPLICATES REMOVED)
L7             1 S L6 NOT L4
                 E GOLDBERG EDWARD?/AU
                 E GOLDBERG EDWAR?/AU
L8            20 S E4
L9            42 S E5
L10           62 S L8 OR L9
L11            6 S L10 AND (P35 OR GP35)
L12            5 DUP REM L11 (1 DUPLICATE REMOVED)
L13            5 SORT L12 PY
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=> d an ti so au ab pi l13 1-5

L13 ANSWER 1 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1996:404766 CAPLUS
DN 125:51926
TI Tail fiber proteins of T-even-like bacteriophage for the production of nanometer structures and use thereof
SO PCT Int. Appl., 82 pp.
CODEN: PIXXD2
IN **Goldberg, Edward B.**
AB Described is the preparation of nanostructures, i.e., nanometer sized structures useful in the construction of microscopic and macroscopic structures, based on bacteriophage T4 tail fiber proteins and variants thereof. Preparation of single or fusion proteins or their variants selected from gp34, **gp35**, gp36, and gp37 of T-4 bacteriophage was demonstrated. Also provided are kits for making nanostructures, comprising purified, e.g., **gp35** and gp36-34 chimer, or gp37-36 chimer.

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9611947	A1	19960425	WO 1995-US13023	19951013
W: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN				
RW: KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5877279	A	19990302	US 1994-322760	19941013
CA 2202474	AA	19960425	CA 1995-2202474	19951013
AU 9538296	A1	19960506	AU 1995-38296	19951013
AU 689662	B2	19980402		
EP 785946	A1	19970730	EP 1995-936297	19951013
EP 785946	B1	20041229		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
BR 9509487	A	19970930	BR 1995-9487	19951013
CN 1168676	A	19971224	CN 1995-196597	19951013
CN 1113068	B	20030702		
HU 77683	A2	19980728	HU 1998-746	19951013
JP 10508194	T2	19980818	JP 1996-513358	19951013
RU 2162856	C2	20010210	RU 1997-107477	19951013
AT 286068	E	20050115	AT 1995-936297	19951013

L13 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1999:69916 CAPLUS
DN 130:135644
TI Use of bacteriophage T4 tail fiber proteins in the preparation of nanostructures
SO U.S., 51 pp., Cont.-in-part of U.S. Ser. No. 322,760.

CODEN: USXXAM

IN **Goldberg, Edward B.**

AB Methods of using the gp34, **gp35**, gp36, and gp37 tail fiber proteins of bacteriophage T4 in the formation of nanostructures that can be used in nanomachines is described. In particular, variants of the proteins that show altered patterns of interaction, thermolability of interaction, or geometry of interaction can be used to create an array of self-assembling structures.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5864013	A	19990126	US 1995-542003	19951012
	US 5877279	A	19990302	US 1994-322760	19941013
	CA 2202474	AA	19960425	CA 1995-2202474	19951013
	CN 1168676	A	19971224	CN 1995-196597	19951013
	CN 1113068	B	20030702		
	HU 77683	A2	19980728	HU 1998-746	19951013
	US 6437112	B1	20020820	US 1999-236949	19990125
	US 2003236390	A1	20031225	US 2002-136225	20020429
	US 2004018587	A1	20040129	US 2003-371067	20030221
	US 2004039168	A1	20040226	US 2003-371073	20030221

L13 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2000:900798 CAPLUS

DN 134:67178

TI Cloning and characterization of phage T4 gene **gp35**

SO PCT Int. Appl., 75 pp.
CODEN: PIXXD2

IN **Goldberg, Edward B.**

AB The invention provides sequences of phage T4 gene **gp35** and its encoded protein and cDNA sequences of a novel human gene which is located between gene gp34 and gene gp36. Gene **gp35** encodes a tail fiber protein which functions to join the rodlike proximal and distal halves of the bacteriophage tail fibers. A thermostable **gp35** mutant protein is also isolated from a ts mutant. The present invention further relates to the use of bacteriophage T4 **gp35** gene and protein products as well as derivs., variants, and analogs thereof in the construction of nanostructures.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000077196	A1	20001221	WO 1999-US13024	19990611
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	CA 2375998	AA	20001221	CA 1999-2375998	19990611
	AU 9946781	A1	20010102	AU 1999-46781	19990611
	EP 1185638	A1	20020313	EP 1999-930192	19990611
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2003507007	T2	20030225	JP 2001-503640	19990611

L13 ANSWER 4 OF 5 MEDLINE on STN

AN 2004603885 MEDLINE

TI In vivo bypass of chaperone by extended coiled-coil motif in T4 tail fiber.

SO Journal of bacteriology, (2004 Dec) 186 (24) 8363-9.
Journal code: 2985120R. ISSN: 0021-9193.

AU Qu Yun; Hyman Paul; Harrah Timothy; **Goldberg Edward**

AB The distal-half tail fiber of bacteriophage T4 is made of three gene products: trimeric gp36 and gp37 and monomeric **gp35**. Chaperone P38 is normally required for folding gp37 peptides into a P37 trimer; however, a temperature-sensitive mutation in T4 (ts3813) that suppresses this requirement at 30 degrees C but not at 42 degrees C was found in gene 37 (R. J. Bishop and W. B. Wood, Virology 72:244-254, 1976). Sequencing of the temperature-sensitive mutant revealed a 21-bp

duplication of wild-type gene 37 inserted into its C-terminal portion (S. Hashemolhosseini et al., J. Mol. Biol. 241:524-533, 1994). We noticed that the 21-amino-acid segment encompassing this duplication in the ts3813 mutant has a sequence typical of a coiled coil and hypothesized that its extension would relieve the temperature sensitivity of the ts3813 mutation. To test our hypothesis, we crossed the T4 ts3813 mutant with a plasmid encoding an engineered pentaheptad coiled coil. Each of the six mutants that we examined retained two amber mutations in gene 38 and had a different coiled-coil sequence varying from three to five heptads. While the sequences varied, all maintained the heptad-repeating coiled-coil motif and produced plaques at up to 50 degrees C. This finding strongly suggests that the coiled-coil motif is a critical factor in the folding of gp37. The presence of a terminal coiled-coil-like sequence in the tail fiber genes of 17 additional T-even phages implies the conservation of this mechanism. The increased melting temperature should be useful for "clamps" to initiate the folding of trimeric beta-helices in vitro and as an in vivo screen to identify, sequence, and characterize trimeric coiled coils.

L13 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:162508 CAPLUS
DN 140:213583
TI Use of bacteriophage T4 tail fiber proteins for manufacture of nanostructures using staged-assembly
SO U.S. Pat. Appl. Publ., 60 pp., Cont.-in-part of U.S. Ser. No. 136,225. CODEN: USXXCO
IN **Goldberg, Edward B.**
AB Methods of using the gp34, gp35, gp36, and gp37 tail fiber proteins of bacteriophage T4 or fusion proteins in the formation of nanostructures that can be used in nanostructures is described. In particular, variants of the proteins that show altered patterns of interaction, thermolability of interaction, or geometry of interaction can be used to create an array of self-assembling structures.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004039168	A1	20040226	US 2003-371073	20030221
	US 5877279	A	19990302	US 1994-322760	19941013
	US 5864013	A	19990126	US 1995-542003	19951012
	US 6197139	B1	20010306	US 1999-226949	19990108
	US 2003236390	A1	20031225	US 2002-136225	20020429

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